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<151> 2003-03-20
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<150> 60/365,527
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Ala Lys Thr Leu Asp Tyr Ala Lys Ala Val Leu His Pro Glu Thr Phe 50 55 60

Asn His Ser Met Arg Val Tyr His Tyr Gly Met Ala Ile Thr Lys Gln 65 70 75 80

Gln Phe Pro Glu Gln Ala Ala Ala Leu Ser Pro Ile Thr Trp Ala Leu 85 90 95

Thr Cys Leu Leu His Asp Leu Gly Thr Ala Glu Glu Asn Leu Thr Ala 100 105 110

Thr Arg Met Ser Phe Asp Ile Tyr Gly Gly Ile Lys Ala Leu Ser Val 115 120 125

Leu Lys Asp Phe Gly Ala Thr Val Asp Gln Ala Glu Ala Ala Glu 130 135 140

Ala Ile Ile Arg His Glu Asp Met Gly Val Asp Gly Thr Ile Thr Tyr 145 150 155 160

Ile Gly Gln Leu Ile Gln Leu Ala Thr Thr Tyr Asp Asn Thr Gly Phe 165 170 175

His Pro His Val Lys Asp Phe Gly Lys Leu Val His Asp Glu Thr Arg 180 185 190

Ala Gln Ile Asn Thr Ala Tyr Pro Arg Leu Lys Trp Cys Thr Phe Phe 195 200 205

Ser Gly Val Ile Arg Lys Glu Glu Thr Ile Lys Pro Trp Cys His Ser 210 215 220

Thr His Leu Val Asp Phe Asp Lys Glu Ile Glu Ala Gly Thr Pro Asp 235 240

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<211> 244

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<213> Myrothecium verrucaria

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Ser Tyr Ser Val Glu Asp Ile Ala Phe Pro Ala Ala Asp Lys Leu Val 35 40 45

Ala Glu Ala Gln Ala Phe Val Lys Ala Arg Leu Ser Pro Glu Thr Tyr
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Asn His Ser Met Arg Val Phe Tyr Trp Gly Thr Val Ile Ala Arg Arg 65 70 75 80

Leu Leu Pro Glu Gln Ala Lys Asp Leu Ser Pro Ser Thr Trp Ala Leu 85 90 95

Thr Cys Leu Leu His Asp Val Gly Thr Ala Glu Ala Tyr Phe Thr Ser 100 105 110

Thr Arg Met Ser Phe Asp Ile Tyr Gly Gly Ile Lys Ala Met Glu Val 115 120 125

Leu Lys Val Leu Gly Ser Ser Thr Asp Gln Ala Glu Ala Val Ala Glu 130 135 140

Ala Ile Ile Arg His Glu Asp Val Gly Val Asp Gly Asn Ile Thr Phe 145 150 155 160

Leu Gly Gln Leu Ile Gln Leu Ala Thr Leu Tyr Asp Asn Val Gly Ala 165 170 175

Tyr Asp Gly Ile Asp Asp Phe Gly Ser Trp Val Asp Asp Thr Thr Arg
180 185 190

Asn Ser Ile Asn Thr Ala Phe Pro Arg His Gly Trp Cys Ser Trp Phe 195 200 205

Ala Cys Thr Val Arg Lys Glu Glu Ser Asn Lys Pro Trp Cys His Thr 210 215 220

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Lys Pro Trp Glu

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<212> PRT

<213> Aspergillus sp.

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Ala Leu Ser Ile Glu Glu Ile Lys Phe Pro Val Asp Asp Pro Ile Val 35 40 45

Glu Lys Thr Met Arg Tyr Ala Lys Ala Ala Leu Pro Thr Glu Thr Phe 50 55 60

Asn His Ser Met Arg Val Tyr Tyr Tyr Gly Met Gln Asp Cys Ala Ser 65 70 75 80

His Gly Val Leu Ile Asn Arg Ser Gln Ala Leu Gly Met Ala Ile Thr 85 90 95

Lys Gln Gln Phe Pro Lys Gln Ala Ser Ala Leu Ser Pro Ser Thr Trp 100 105 110

Ala Leu Thr Cys Leu Leu His Asp Ile Gly Thr Ser Asp His Asn Leu 115 120 125

Ala Ala Thr Arg Met Ser Phe Asp Ile Tyr Gly Gly Ile Lys Ala Leu 130 135 140

Glu Val Leu Lys Gly Phe Gly Ala Thr Ser Asp Gln Ala Glu Ala Val 145 150 155 160

Ala Glu Ala Ile Ile Arg His Gln Asp Leu Gly Val His Gly Thr Ile 165 170 175

Thr Tyr Ile Gly Gln Leu Ile Gln Leu Ala Thr Ile Tyr Asp Asn Val 180 185 190

Gly Ala His Pro Tyr Val Lys Asp Phe Gly Glu Leu Ile His Asp Thr 195 200 205

Thr Arg Ser Gln Val His Glu Ala His Pro Pro Gly Glu Trp Arg Thr 210 220

Phe Phe Ser Gly Val Ile Gln Lys Glu Gln Ala Ile Lys Pro Trp Cys 235 240

His Thr Lys Lys Met Val Asn Val Leu Arg Lys Gly Ser Arg His Pro
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Asp Gly Gln

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<213> Saccharomyces cerevisiae

<400> 23

Met Ser Gln Tyr Gly Phe Val Arg Val Pro Arg Glu Val Glu Lys Ala 1 5 10 15

Ile Pro Val Val Asn Ala Pro Arg Pro Arg Ala Val Val Pro Pro Pro 20 25 30

Asn Ser Glu Thr Ala Arg Leu Val Arg Glu Tyr Ala Ala Lys Glu Leu 35 40 45

Thr Ala Pro Val Leu Asn His Ser Leu Arg Val Phe Gln Tyr Ser Val
50 - 55 60

Ala Ile Ile Arg Asp Gln Phe Pro Ala Trp Asp Leu Asp Gln Glu Val 65 70 75 80

Leu Tyr Val Thr Cys Leu Leu His Asp Ile Ala Thr Thr Asp Lys Asn 85 90 95

Met Arg Ala Thr Lys Met Ser Phe Glu Tyr Tyr Gly Gly Ile Leu Ser 100 105 110

Arg Glu Leu Val Phe Asn Ala Thr Gly Gly Asn Gln Asp Tyr Ala Asp 115 120 125

Ala Val Thr Glu Ala Ile Ile Arg His Gln Asp Leu Thr Gly Thr Gly 130 135 140

Tyr Ile Thr Thr Leu Gly Leu Ile Leu Gln Ile Ala Thr Thr Leu Asp 145 150 155 160

Asn Val Gly Ser Asn Thr Asp Leu Ile His Ile Asp Thr Val Ser Ala 165 170 175

Ile Asn Glu Gln Phe Pro Arg Leu His Trp Leu Ser Cys Phe Ala Thr 180 185 190

Val Val Asp Thr Glu Asn Ser Arg Lys Pro Trp Gly His Thr Ser Ser 195 200 205

Leu Gly Asp Asp Phe Ser Lys Lys Val Ile Cys Asn Thr Phe Gly Tyr 210 215 220

Asn

225

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<211> 274

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ctttttccgc ggaattgcgc ggtggggacg gattccacaa ccgcgacgca accgcctctc 180
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cttcccggaa accgcggtgg tttcagcgtg gcggattccc cctcccacca cccaaccgcc 180
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